AMENDMENTS TO THE SPECIFICATION

Before paragraph 1, please insert the following:

--CROSS REFERENCE TO RELATED APPLICATIONS

This application is a 371 national stage application of PCT/US2003/040101 and claims priority to and benefit of USSN 60/433,045.—

Please amend the brief description of the drawings at page 2-3 as indicated:

Figure 1 Diagrammatic representation of the human DRD4 gene region. Exon positions are indicated by blocks (~~yellow~~ open box: noncoding, ~~orange~~ hatched: coding). The approximate positions of a 120bp promoter region duplication (~~blue~~ triangle), an exon 1 12bp duplication (~~blue~~ triangle), an exon 3 48bp VNTR (~~blue~~ triangle), and two intron 3 SNPs are indicated. 2R through 11R variants of the 48bp VNTR are indicated below exon 3 ~~(blue)~~, along with their worldwide population frequencies determined by PCR analysis (3,17).

Figure 2 Nucleotide and amino acid sequences of VNTR motifs. The nucleotide and corresponding amino acid ~~(red)~~ sequences of 35 DRD4 exon 3 48bp repeat motifs (SEQ ID NO: 1-35) are shown. Prior nomenclature (2) for 19 of these motifs are indicated (α through ξ). The putative single step origin of most of these motifs is indicated, either as a recombination event (R) or a mutation event (M). For example, the seven motif is hypothesized to be a recombination between a 2 motif and a 3 motif (R 2/3) and the 8 motif is hypothesized to be a single point mutation of a 2 motif (M 2). Motifs 1 though 6, which account for the vast majority of observed haplotype variants (Table 1), are considered the progenitors. Motifs with no putative origin noted (for example, motif 15), have multiple possible progenitors.